

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:42:07 ; Search time 13 Seconds
 (without alignments)

19.585 Million cell updates/sec

Title: US-10-634-895-3

Perfect score: 172

Sequence: 1 PHVNGLETRTETWNSSEGAWKHYQRIETW 30

Scoring table: Blosum62

Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New; *

1: /cgm2_6/ptodata/2/pubaa/US08_NEW_PUB.PEP; *

2: /cgm2_6/ptodata/2/pubaa/US06_NEW_PUB.PEP; *

3: /cgm2_6/ptodata/2/pubaa/US07_NEW_PUB.PEP; *

4: /cgm2_6/ptodata/2/pubaa/PCT_NEW_PUB.PEP; *

5: /cgm2_6/ptodata/2/pubaa/US09_NEW_PUB.PEP; *

6: /cgm2_6/ptodata/2/pubaa/US10_NEW_PUB.PEP; *

7: /cgm2_6/ptodata/2/pubaa/US11_NEW_PUB.PEP; *

8: /cgm2_6/ptodata/2/pubaa/US60_NEW_PUB.PEP; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	48	27.9	192	6 US-10-981-873-43	Sequence 43, App1
2	47.5	27.6	3674	7 US-11-000-463-454	Sequence 454, App
3	46	26.7	334	6 US-10-793-626-282	Sequence 282, App
4	45.5	26.5	750	7 US-11-132-285-2	Sequence 2, App1
5	45.5	26.5	1001	7 US-11-132-285-40	Sequence 40, App1
6	45.5	26.5	1013	6 US-10-131-826A-38	Sequence 38, App1
7	44.5	25.9	662	7 US-11-091-439-9	Sequence 9, App1
8	44	25.6	407	7 US-11-127-877-56	Sequence 56, App1
9	44	25.6	573	6 US-10-525-710-36	Sequence 36, App1
10	43	25.3	218	6 US-10-793-626-562	Sequence 562, App
11	43.5	25.3	792	7 US-11-108-172-1127	Sequence 1127, App
12	43	25.0	192	7 US-11-055-822-206	Sequence 204, App
13	43	25.0	192	7 US-11-055-822-250	Sequence 250, App
14	43	25.0	200	7 US-11-055-822-204	Sequence 204, App
15	43	25.0	200	7 US-11-055-822-248	Sequence 248, App
16	43	25.0	275	7 US-11-107-028-23	Sequence 23, App1
17	43	25.0	437	6 US-10-858-730-214	Sequence 214, App
18	43	25.0	437	6 US-10-858-730-283	Sequence 283, App
19	43	25.0	437	6 US-10-858-730-288	Sequence 288, App
20	43	25.0	480	6 US-10-510-386-12	Sequence 12, App1
21	43	25.0	841	7 US-11-052-554A-102	Sequence 102, App
22	43	25.0	873	6 US-10-793-626-3036	Sequence 3036, App
23	43	25.0	1070	7 US-11-000-463-721	Sequence 721, App
24	43	25.0	1194	7 US-11-000-463-249	Sequence 249, App
25	42	24.4	684	6 US-10-714-781A-55	Sequence 55, App1

ALIGNMENTS

RESULT 1
 US-10-981-873-43
 ; Sequence 43, Application US/10981873
 ; Publication No. US2005025068041
 ; GENERAL INFORMATION:
 ; APPLICANT: Walensky, Loren D.
 ; APPLICANT: Korsmeyer, Stanley J.
 ; APPLICANT: Verdina, Gregory
 ; TITLE OF INVENTION: SUBSTITUTED ALPHA HELICAL PEPTIDES AND
 ; THERAPY THEREOF
 ; FILE REFERENCE: 00530-124001
 ; CURRENT APPLICATION NUMBER: US/10/981,873
 ; CURRENT FILING DATE: 2004-11-05
 ; PRIORITY APPLICATION NUMBER: US 60/517,848
 ; PRIORITY FILING DATE: 2003-11-05
 ; PRIORITY APPLICATION NUMBER: US 60/591,548
 ; PRIORITY FILING DATE: 2004-07-27
 ; NUMBER OF SEQ ID NOS: 117
 ; SOFTWARE: FastSeqQ for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 192
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; US-10-981-873-43

Query Match 27.9%; Pred. No. 3.5%; Mismatches 1; Indels 0; Gaps 0;

QY 7 LETRTEETMSSEGAW 21
 Db 129 LETRLADWTHSSGGW 143

RESULT 2
 US-11-000-463-454
 ; Sequence 454, Application US/11000463
 ; Publication No. US2005026423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Chen, Rui-nong
 ; APPLICANT: Qian, Xiaohong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Zhou, Ping

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Om protein - protein search, using sw model

Run on: January 4, 2006, 18:38:57 ; Search time 164 Seconds

(without alignments)
76.432 Million Cell updates/sec

Title: US-10-634-895-3

Perfect score: 172

Sequence: 1 PHVNGCLETRTETWNSSEGAWKHYORIETW 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41782936 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main.*

1: /cmn2_6_ptodata/1/pubpa/us01_pubcomb.pep:*
2: /cmn2_6_ptodata/1/pubpa/us08_pubcomb.pep:*
3: /cmn2_6_ptodata/1/pubpa/us09_pubcomb.pep:*
4: /cmn2_6_ptodata/1/pubpa/us10_pubcomb.pep:*
5: /cmn2_6_ptodata/1/pubpa/us11_pubcomb.pep:*
6: /cmn2_6_ptodata/1/pubpa/us11_pubcomb.pep:*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	172	100.0	30	3 US-09-881-710-3	Sequence 3, Appli
2	172	100.0	30	3 US-09-881-710-11	Sequence 11, Appli
3	172	100.0	30	4 US-10-634-895-3	Sequence 3, Appli
4	172	100.0	30	4 US-10-634-895-11	Sequence 11, Appli
5	172	100.0	40	5 US-10-608-147-31	Sequence 31, Appli
6	172	100.0	48	4 US-10-311-13-32	Sequence 32, Appli
7	172	100.0	48	5 US-10-608-029-35	Sequence 35, Appli
8	172	100.0	685	5 US-10-500-796A-43	Sequence 43, Appli
9	172	100.0	685	5 US-10-500-796A-45	Sequence 47, Appli
10	172	100.0	685	5 US-10-500-796A-47	Sequence 47, Appli
11	168	97.7	40	3 US-09-881-710-29	Sequence 29, Appli
12	168	97.7	40	4 US-10-634-895-29	Sequence 29, Appli
13	168	97.7	167	4 US-10-375-932-122	Sequence 122, Appli
14	168	97.7	171	4 US-10-375-932-118	Sequence 118, Appli
15	168	97.7	171	4 US-10-375-932-121	Sequence 121, Appli
16	168	97.7	675	4 US-10-375-932-143	Sequence 143, Appli
17	168	97.7	677	4 US-10-375-932-238	Sequence 238, Appli
18	168	97.7	681	4 US-10-375-932-142	Sequence 142, Appli
19	168	97.7	681	4 US-10-375-932-228	Sequence 228, Appli
20	168	97.7	1127	4 US-10-247-960-3	Sequence 3, Appli
21	168	97.7	3388	5 US-10-719-547-17	Sequence 17, Appli
22	168	97.7	3391	5 US-10-719-547-21	Sequence 21, Appli
23	168	97.7	3391	5 US-10-871-775-31	Sequence 31, Appli
24	163	94.8	678	4 US-10-375-932-248	Sequence 248, Appli
25	162	94.2	661	4 US-10-701-122-51	Sequence 51, Appli
26	160	93.0	40	4 US-10-311-213-3	Sequence 3, Appli
27	160	93.0	677	4 US-10-375-932-345	Sequence 345, Appli

ALIGNMENTS

RESULT 1
US-09-881-710-3
; Sequence 3, Application US/09881710
; Publication No. US2002008403A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; DEBUEL, Vincent
; APPLICANT: CATIEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09-881-710-12
; CURRENT FILING DATE: 2001-06-18
; PRIORITY APPLICATION NUMBER: 60/212,129
; PRIORITY FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Dengue virus
US-09-881-710-3

Query Match 100.0% ; Score 172 ; DB 3 ; Length 30;
Best Local Similarity 100.0% ; Pred. No. 5 ; e-16;
Matches 30 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY 1 PHVNGCLETRTETWNSSEGAWKHYORIETW 30
Db 1 PHVNGCLETRTETWNSSEGAWKHYORIETW 30

RESULT 2
US-09-881-710-11
; Sequence 11, Application US/09881710
; Publication No. US2002008403A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; CATIEAU, Adeline
; APPLICANT: DESPRES, Philippe
; DEBUEL, Vincent
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09-881-710-12
; CURRENT FILING DATE: 2001-06-18
; PRIORITY APPLICATION NUMBER: 60/212,129
; PRIORITY FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11

Result No.	Score	Query	Match	Length	DB	ID	Description
1	172	100.0	30	2	US-09-881-710-3	Sequence 3, App1	Sequence 3, App1
2	172	100.0	30	2	US-09-881-710-11	Sequence 1, App1	Sequence 1, App1
3	168	97.7	40	2	US-09-881-710-29	Sequence 29, App1	Sequence 29, App1
4	168	97.7	635	2	US-09-341-833A-7	Sequence 7, App1	Sequence 7, App1
5	168	97.7	677	2	US-09-341-833A-8	Sequence 8, App1	Sequence 8, App1
6	168	97.7	1127	2	US-08-937-195-3	Sequence 3, App1	Sequence 3, App1
7	168	97.7	1127	2	US-08-911-152-3	Sequence 3, App1	Sequence 3, App1
8	168	97.7	1127	2	US-09-376-163-3	Sequence 3, App1	Sequence 3, App1
9	168	97.7	1127	4	PCT-US2006-07627-3	Sequence 3, App1	Sequence 3, App1
10	162	94.2	661	2	US-09-452-638-51	Sequence 51, App1	Sequence 51, App1
11	162	94.2	661	2	US-09-121-587A-2	Sequence 2, App1	Sequence 2, App1
12	156	90.7	39	2	US-09-881-710-12	Sequence 12, App1	Sequence 12, App1
13	156	90.7	40	2	US-09-881-710-28	Sequence 28, App1	Sequence 28, App1
14	156	90.7	76	2	US-09-881-710-1	Sequence 1, App1	Sequence 1, App1
15	152	88.4	635	2	US-09-341-833A-9	Sequence 9, App1	Sequence 9, App1
16	140	81.4	39	2	US-09-881-710-30	Sequence 30, App1	Sequence 30, App1
17	116	67.4	22	2	US-09-341-833A-5	Sequence 5, App1	Sequence 5, App1
18	107	62.2	20	2	US-09-881-710-15	Sequence 15, App1	Sequence 15, App1
19	102	59.3	20	2	US-09-881-710-17	Sequence 17, App1	Sequence 17, App1
20	85	49.4	20	2	US-09-881-710-16	Sequence 16, App1	Sequence 16, App1
21	53	30.8	140	2	US-09-767-47302	Sequence 47302, A	Sequence 47302, A
22	53	30.8	285	2	US-09-251-991A-25160	Sequence 25160, A	Sequence 25160, A
23	52.5	30.5	303	2	US-09-172-914-2	Sequence 2, App1	Sequence 2, App1
24	52.5	30.5	303	2	US-09-766-916-2	Sequence 2, App1	Sequence 2, App1
25	52.5	30.5	303	2	US-09-766-889-2	Sequence 2, App1	Sequence 2, App1
26	52.5	30.5	303	2	US-09-337-040C-2	Sequence 2, App1	Sequence 2, App1
27	52.5	30.5	303	2	US-10-306-249-2	SEQ ID NO 11	SEQ ID NO 11

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OM protein - protein search, using SW model

Run on: January 4, 2006, 18:33:21 ; Search time 227 Seconds
(without alignments)
93.242 Million cell updates/sec

Title: US-10-634-895-3
perfect score: 172
Sequence: 1 PHVNGLETTETTWSSEGAWKHWQRIETW 30

Scoring table: BLASTM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80:
1: uniprot_sprot:
2: uniprot_trembl:
* [1]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	172	100.0	280	2	Q8Q264_9FLAV	Q8z264 dengue virus
2	172	100.0	280	2	Q8Q265_9FLAV	Q8z265 dengue virus
3	172	100.0	280	2	Q8Q266_9FLAV	Q8z266 dengue virus
4	172	100.0	280	2	Q8Q267_9FLAV	Q8z267 dengue virus
5	172	100.0	661	2	Q5V187_9FLAV	Q5i187 dengue virus
6	172	100.0	661	2	Q5V188_9FLAV	Q5i188 dengue virus
7	172	100.0	661	2	Q5V189_9FLAV	Q5i189 dengue virus
8	172	100.0	661	2	Q5V190_9FLAV	Q5i190 dengue virus
9	172	100.0	661	2	Q5V191_9FLAV	Q5i191 dengue virus
10	172	100.0	716	2	Q6D0V2_9FLAV	Q6duv2 dengue virus
11	172	100.0	757	2	Q5SSP1_9FLAV	Q5s8p1 dengue virus
12	172	100.0	757	2	Q5SSP2_9FLAV	Q5s8p2 dengue virus
13	172	100.0	763	2	Q6DUD9_9FLAV	Q6du9 dengue virus
14	172	100.0	775	2	Q5ICU8_9FLAV	Q5icu8 dengue virus
15	172	100.0	775	2	Q66398_9FLAV	Q66398 dengue virus
16	172	100.0	775	2	Q8Q107_9FLAV	Q8y107 dengue virus
17	172	100.0	3391	1	POLG_DEN26	P29990 d genome po
18	172	100.0	3391	1	POLG_DEN27	P29991 d genome po
19	172	100.0	3391	1	POLG_DEN27	P07564 d genome po
20	172	100.0	3391	2	009234_DEN26	009234 dengue virus
21	172	100.0	3391	2	011875_9FLAV	011875 dengue virus
22	172	100.0	3391	2	Q5B167_9FLAV	Q5by167 dengue virus
23	172	100.0	3391	2	Q5B169_9FLAV	Q5by169 dengue virus
24	172	100.0	3391	2	Q5B171_9FLAV	Q5by171 dengue virus
25	172	100.0	3391	2	Q8Q227_9FLAV	Q8y227 dengue virus
26	172	100.0	3391	2	Q91094_9FLAV	Q9i1094 dengue virus
27	172	100.0	3391	2	Q68126_9FLAV	Q68126 dengue virus
28	172	100.0	3391	2	Q68130_9FLAV	Q68130 dengue virus
29	168	97.7	120	2	Q67424_9FLAV	Q67424 dengue virus
30	168	97.7	166	2	Q66346_9FLAV	Q66346 dengue virus
31	168	97.7	661	2	Q5Q1B6_9FLAV	Q5q1b6 dengue virus

ALIGNMENTS

RESULT 1 Q8Q264_9FLAV PRELIMINARY;						
ID	AC	PRT;	280 AA.			
Q8Q264_9FLAV						
ID	Q8Q264_					
DT	01-JUN-2002	(TREMBLrel.)	21, Created)			
DT	01-JUN-2002	(TREMBLrel.)	21, Last sequence update)			
DT	01-JUN-2003	(TREMBLrel.)	24, Last annotation update)			
DB	Polyprotein (fragment).					
OS	Dengue virus type 2.					
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;					
OX	Flavivirus; Dengue virus group.					
RN	NCBP1_TREMBL SEQUENCE.					
RP	NUCLEOTIDE SEQUENCE.					
DR	EMBL; AF360863; AAL76291.1; -; Genomic; RNA.					
DR	SNMPL; Q80Z64; 21-100					
DR	GO; GO-0019028; C:viral capsid, IEA.					
DR	GO; GO-0005198; F:structural molecule activity; IEA.					
DR	GO; GO-0019058; P:viral infectious cycle; IEA.					
DR	InterPro; IPR000069; Flavi M.					
DR	InterPro; IPR002535; Flavi Propep.					
DR	Pram; PF01003; Flavi capsid; 1.					
DR	PFam; PF01004; Flavi M; 1.					
DR	PFam; PF01040; Flavi_propep; 1.					
KW	Polyprotein.					
FT	NON_TER	280	280 AA;	31846_MW;	E889FDD11929CBA7 CRC64;	
SQ	SEQUENCE	280	280 AA;	31846_MW;	E889FDD11929CBA7 CRC64;	
Query	Match	100.0%	Score 172;	DB 2;	Length 280;	
Best Local Similarity	100.0%		Score 172;	DB 2;	Length 280;	
Matches	30;	Conservative	0;	Mismatches	0;	Indels 0;
						Gaps 0;
Qy	1 PHVGMLGLTRTRTWTMSSEGAWKHWQRIETW 30					
Db	211 PHVGMLGLTRTRTWTMSSEGAWKHWQRIETW 240					
Result 2	Q8Q265_9FLAV					
ID	Q8Q265_	9FLAV				
AC	Q8Q265;					
DT	01-JUN-2002	(TREMBLrel.)	21, Created)			
DT	01-JUN-2002	(TREMBLrel.)	21, Last sequence update)			
DR	EMBL; AF360863; AAL76291.1; -; Genomic; RNA.					
DR	SNMPL; Q80Z65; 21-100					
DR	GO; GO-0019028; C:viral capsid, IEA.					
DR	GO; GO-0005198; F:structural molecule activity; IEA.					
DR	GO; GO-0019058; P:viral infectious cycle; IEA.					
DR	InterPro; IPR000069; Flavi M.					
DR	InterPro; IPR002535; Flavi Propep.					
DR	Pram; PF01003; Flavi capsid; 1.					
DR	PFam; PF01004; Flavi M; 1.					
DR	PFam; PF01040; Flavi_propep; 1.					
KW	Polyprotein.					
FT	NON_TER	280	280 AA;	31846_MW;	E889FDD11929CBA7 CRC64;	
SQ	SEQUENCE	280	280 AA;	31846_MW;	E889FDD11929CBA7 CRC64;	
Query	Match	100.0%	Score 172;	DB 2;	Length 280;	
Best Local Similarity	100.0%		Score 172;	DB 2;	Length 280;	
Matches	30;	Conservative	0;	Mismatches	0;	Indels 0;
						Gaps 0;

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:34:31 : Search time 37 Seconds
(without alignments)

78.014 Million cell updates/sec

Title: US-10-634-895-3

Perfect score: 172

Sequence: 1 PHVGMGLERTRTTWMSSEGAWKHYQRIETW 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_80;*

1: PIR1;*

2: PIR2;*

3: PIR3;*

4: PIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	172	100.0	775	2	A48644	polyprotein - deng genome polyprotein
2	172	100.0	3391	1	GNWV16	genome polyprotein
3	172	100.0	3391	1	GNWV26	genome polyprotein
4	172	100.0	3391	1	GNWVJA	prenmembrane protein
5	168	97.7	166	2	S01144	genome polyprotein
6	168	97.7	3388	1	GNWVDP	polyprotein - deng genome polyprotein
7	168	97.7	3391	2	JS0119	genome polyprotein
8	162	94.2	665	2	PS0043	genome polyprotein
9	159	92.4	3396	1	A42551	membrane protein
10	158	91.9	166	2	S09223	polyprotein(C, E)
11	156	90.7	775	2	C32401	genome polyprotein
12	156	90.7	792	2	B32401	genome polyprotein
13	156	90.7	792	2	A32401	membrane protein - structural polyprotein
14	156	90.7	792	2	GNWVDP	genome polyprotein
15	156	90.7	1226	1	S09224	membrane protein
16	154	89.5	166	2	S09225	structural polyprotein
17	154	89.5	88.4	2	A47666	genome polyprotein
18	152	88.4	773	2	GNWVDF	membrane protein
19	152	88.4	3386	1	GNWVDS	membrane-associated protein M; nonstructural protein NS4b; nonstructural protein NS5
20	145	84.3	3390	1	GNWVTD2	membrane-associated protein M; nonstructural protein NS5
21	139	80.8	1127	1	GNWVYB	membrane-associated protein M; nonstructural protein NS5
22	68	39.5	1163	1	GNWVYV	membrane-associated protein M; nonstructural protein NS5
23	68	39.5	3411	1	GNWVYP	membrane-associated protein M; nonstructural protein NS5
24	54.5	31.7	636	2	A87134	methylmalonyl-CoA hydroxylase
25	54.5	31.7	193	2	T08300	hypothetical protein
26	54	31.4	1127	2	G71274	hypothetical protein
27	54	31.4	132	2	P82663	hypothetical protein
28	53.5	31.1	340	2	C71266	conserved by hypothet
29	53	30.8	2			

ALIGNMENTS

RESULT 1						
A48644	polypeptide - dengue virus type 2 (strain Mexican) (fragment)					
C;Species: dengue virus type 2						
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 31-Dec-2004						
C;Accession: A48644						
R;Ruiz, B.H.; Sanchez, I.; Ortega, G.J.; Lopez, I.; Ortiz-Ortiz, L.						
R;Submitted to GenBank, October 1992						
A;Description: Nucleotide sequence and deduced amino-acid sequence of the structural protein						
A;Reference number: A48644						
A;Status: preliminary						
A;Molecule type: genomic RNA						
A;Cross-references: UNIPROT:Q66398; UNIPARCL00000BBB45; GB:L04561; PMID:9323652; PIDN:9323652						
A;Residues: 1-775 <RUI>						
C;Superfamily: hepatitis C virus genome polyprotein						
C;Keywords: polyprotein						
Query Match						
1	PHVGMLGLERTRTTWMSSEGAWKHYQRIETW	30	100.0%	Score 172;	DB 2;	Length 775;
Qy			Best Local Similarity	100.0% ; Pred. No. 1.4e-15;		
Db			Matches 30; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;		
			1 PHVGMLGLERTRTTWMSSEGAWKHYQRIETW	240		
RESULT 2						
GNWV16	genome polyprotein - dengue virus type 2 (strain 16681)					
N;Contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstructural protein NS4A; nonstructural protein NS4b; nonstructural protein NS5						
C;Species: dengue virus type 2						
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004						
C;Accession: A42451; A42496; A47363						
R;Blok, J.; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Weiller, G.; Herring, B.L.; Hemmingsen, T.; Virology 187, 573-590, 1992						
A;Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence analysis						
A;Reference number: A42451; PMID:1312269						
A;Molecule type: genomic RNA						
A;Cross-references: UNIPROT:P29990; UNIPARCL00001310P5; GB:M84727; GB:M85259; NID:93						
C;Superfamily: hepatitis C virus genome polyprotein						
C;Keywords: ARP; capsid protein; envelope protein; glycoprotein; nonstructural protein						
F;1-114<Product: capsid protein C #status Predicted <CPO>						
F;115-280<Product: membrane-associated protein M precursor #status Predicted <MP>						
F;115-405<Domain: nonterminal signal sequence #status Predicted <SIG>						
A;Accession: A42451						
A;Residues: 1-3391 <BLO>						

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:32:23 ; Search time 186 Seconds
(without alignments)
70.868 Million cell updates/sec

Title: US-10-634-895-3

Perfect score: 172

Sequence: 1 PHVNGGLETRTETMSSGAWKHVRQIETW 30

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 2443163 seqs, 419378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqP1980b;*
- 2: geneseqP1990b;*
- 3: geneseqP2000b;*
- 4: geneseqP2001b;*
- 5: geneseqP2002b;*
- 6: geneseqP2003ab;*
- 7: geneseqP2003bb;*
- 8: geneseqP2004b;*
- 9: geneseqP2005b;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	172	100.0	48	5	AAB17433	Aae17433 (95-114)E
2	172	100.0	48	9	ADW12588	Adw12588 P(95-114)
3	172	100.0	685	6	ABP57874	Abp57874 Plasmid P
4	172	100.0	685	6	ABP57876	Abp57876 Plasmid P
5	172	100.0	685	6	ABP57875	Abp57875 Plasmid P
6	172	100.0	3391	2	AAW06591	Aaw06591 Polyprote
7	172	100.0	3391	2	AAW06590	Aaw06590 Polyprote
8	172	100.0	3391	4	Aae07987	Aae07987 Attenuate
9	172	100.0	3391	4	Aae07986	Aae07986 Wild-type
10	169	98.3	3391	2	AAR13166	Aar13166 Proteins
11	168	97.7	40	5	AAB17432	Aae17432 Dengue vi
12	168	97.7	167	8	ADN37497	Adn37497 Dengue vi
13	168	97.7	171	8	ADN37493	Adn37493 Dengue vi
14	168	97.7	171	8	ADN37496	Adn37496 Dengue vi
15	168	97.7	635	2	ARW55410	Arw55410 Fusion pr
16	168	97.7	675	8	ADN37518	Adn37518 Dengue vi
17	168	97.7	677	2	AAW75411	Aaw75411 Fusion pr
18	168	97.7	677	8	ADN37613	Adn37613 Dengue vi
19	168	97.7	681	8	ADN37603	Adn37603 Dengue vi
20	168	97.7	681	8	ADN37517	Adn37517 Dengue vi
21	168	97.7	1127	2	AAW06409	Aaw06409 Dengue vi
22	168	97.7	1127	2	AAW05522	Aaw05522 Dengue vi
23	168	97.7	1127	7	ADL98086	Adl98086 Dengue vi
24	168	97.7	1127	8	ADQ28716	Adq28716 Dengue vi

ALIGNMENTS

RESULT 1
AAB17433

ID AAB17433 standard; protein; 48 AA.

ID XX

AC XX

DT 18-APR-2002

(first entry)

DB (95-114)EGFP (206-245)DEN-2 fusion protein.

KW Dengue virus; PRM glycoprotein; E glycoprotein; apoptosis; virucide; cancer; flavivirus infection; cyostatic; EGFP; DEN-2 protein; enhanced green fluorescent protein; fusion protein; M ectodomain.

KW Dengue virus; 2.

KW Dengue virus; 1.

KW Unidentified.

KW Chimeric.

Location/Qualifiers
PH Key
FT Misc-difference 13...44
/note= "Encoded by GTTATC"

XX WO200196376-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-IB001570.

XX 16-JUN-2000; 2000US-0212129P.

XX (INSP) INST PASTEUR.

XX Despres P, Courageot M, Deubal V, Catteau A;

XX PI

XX DR

XX N-PSDB; AAD27335.

XX Novel apoptosis inducing polypeptide fragments of Dengue virus-1 or 2 M

PT Protein, useful for inducing apoptosis in a cell of a human patient suffering from cancer or flavivirus infection.

PT Claim 42; Fig 11; 45pp; English.

CC The invention relates to pro-apoptotic fragments of the Dengue virus (DEN) PRM and E glycoproteins, methods for screening molecules capable of inducing apoptosis in a cell. The CC inducing apoptosis and methods of inducing apoptosis in a cell.